In the Specification:

Please amend the specification as shown:

Please delete the paragraph on page 9, line 29, through page 11, line 9, and replace it with the following paragraph:

A 2 cm hair shaft from each species containing no hair root was added to a 2 ml microcentrifuge tube. One milliliter of 5% Terg-a-zyme in deionized water was added to the hair shaft and incubated in a sonicating water bath at room temperature for 20 minutes. The Terg-a-zyme wash solution was discarded and 1 ml of 100% ethanol was added to the hair shaft, covering it entirely. The hair shaft was soaked for 5 minutes in the ethanol and then as much ethanol as possible was removed using a disposable pipette. Fifty microliters of Lysis Reagent (1.8 M NaOH, 25 mM sodium gluconate, 25 mM sodium silicate, 75 mM sodium phosphate) was added to each tube containing a hair shaft and a pipette tip was used to push the hair shaft into the liquid at the bottom of the tube. The hair shaft was incubated in Lysis Buffer for 10 minutes at 60°C and the tubes were vortexed briefly after five minutes and at the end of the 10 minute incubation to facilitate physical disruption of the hair. Six hundred milliliters of Binding Buffer containing 4.2 M guanidine hydrochloride, 0.6 M acetic acid, and 0.9 M potassium acetate, pH 4.4 was added to the digested hair sample and mixed thoroughly by vortexing. Each sample was added to a DNA Binding Column sitting in a receiver tube containing a silica membrane and centrifuged for 1 minute at 12,000 x g. The column flow through was discarded and the column was replaced in the receiver tube. Seven hundred microliters of Wash Solution comprising 1M guanidine and 60% ethanol was added to the column and incubated for 2 minutes at room temperature. The column was then centrifuged for 1 minute at 12,000 x g. The receiver tube was discarded and the DNA Binding Column was placed in a clean receiver tube. Elution buffer comprising 10 mM Tris, 1 mM EDTA, pH 8.0 was heated to 65°C and 75 microliters of the heated Elution Buffer was applied to the center of the silica membrane and incubated for 1 minute. The column was centrifuged for 1 minute at 12,000 x g and the flow-through containing purified mitochondrial DNA was collected in the receiver tube and stored at –20°C. A comparison of the method of the invention to the procedure of Wilson et al for purification of mitochondrial DNA from hair shafts is shown in Figure 1. The purified mitochondrial DNA was amplified by the polymerase chain reaction using the following primer sequences: human, forward primer - CCCCATGCTTACAAGCAAGT **(SEQ ID NO:**

1); human, reverse primer – TGGCTTTATGTACTATGTAC **(SEQ ID NO: 2)**; dog, forward primer – GAACTAGGTCAGCCCGGTACTT **(SEQ ID NO: 3)**, dog, reverse primer – CGGAGCACCAATTATTAACGGC **(SEQ ID NO: 4)**; cat, forward primer – TTCTCAGGATATACCCTTGACA **(SEQ ID NO: 5)**; cat, reverse primer - GAAAGAGCCCATTGAGGAAATC **(SEQ ID NO: 6)** and horse, forward primer- CCCTAAGCCTCCTAATCCGT **(SEQ ID NO: 7)**; horse, reverse primer - AGGAATGATGGGGCAAGTAA **(SEQ ID NO: 8)**. PCR reaction mixes contained 20 mM Tris-HCl (pH 8.4), 1.5 mM MgCl2, 200 uM each dNTP, 200nM each primer, and 1 unit of Platinum Taq Polymerase (Invitrogen Corporation). The template mitochondrial DNA was denatured for 10 minutes at 95°C, and then amplified with 35 cycles of 94°C denaturation for 30 seconds, 55°C primer annealing for 30 seconds, and 72°C primer annealing for 1 minute. At the completion of the 35 cycles, the reactions were extended at 72°C for an additional 1 minute. PCR reactions were separated by agarose gel electrophoresis and DNA bands were visualized by ethidium bromide staining. Bands of the expected size were detected for each of the hair shafts that were processed, and no staining was evident in the negative controls. (see Figure 2.)